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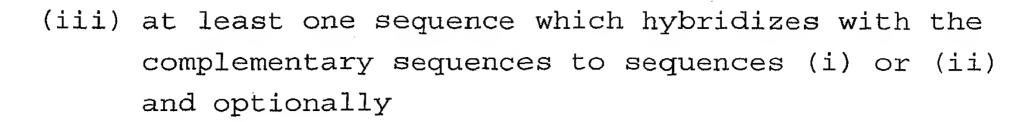


What is claimed is:

An isolated polynucleotide containing a polynucleotide sequence selected from the group consisting of

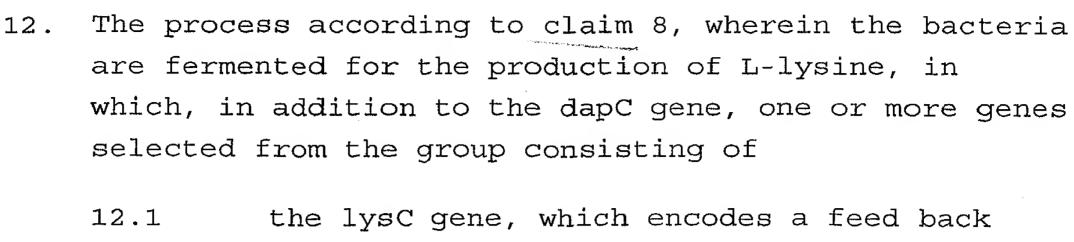
- a) a polynucleotide which is at least 70% identical to a polynucleotide which encodes a polypeptide containing the amino acid sequence of SEQ ID no. 2,
- b) a polynucleotide which encodes a polypeptide which contains an amino acid sequence which is at least 70% identical to the amino acid sequence of SEQ ID no. 2,
  - c) a polynucleotide which is complementary to the polynucleotides of a) or b), and
  - d) a polynucleotide containing at least 15 successive nucleotides of the polynucleotide sequences of a), b) or c).
- 2. The polynucleotide according to claim 1, wherein the polynucleotide is a preferably recombinant DNA replicable in coryneform bacteria.
- 20 3. The polynucleotide according to claim 1, wherein the polynucleotide is an RNA.
  - 4. The polynucleotide according to claim 2, containing the nucleic acid sequence as shown in SEQ ID no. 1.
- 5. The polynucleotide according to claim 2 that is a replicable DNA containing
  - (i) the nucleotide sequence shown in SEQ ID no. 1, or
  - (ii) at least one sequence which matches the sequences(i) within the degeneration range of the genetic code, or

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- (iv) functionally neutral sense mutations in (i).
- 5 6. A vector containing the polynucleotide according to claim 1, in particular pXT-dapCexp, which is characterized by the restriction map shown in Figure 2, deposited under the designation DSM 13254 in Corynebacterium glutamicum.
- 10 7. Coryneform bacteria acting as host cell which contain the vector according to claim 6 or in which the zwal gene is enhanced.
- A process for the production of L-amino acids, in particular L-lysine, wherein the following steps are performed:
  - a) fermentation of the bacteria producing the desired L-amino acid bacteria, in which at least the dapC gene is enhanced,
  - b) accumulation of the desired product in the medium or in the cells of the bacteria, and
  - c) isolation of the L-amino acid.
  - 9. The process according to claim 8, wherein the bacteria are used in which further genes of the biosynthetic pathway of the desired L-amino acid are additionally enhanced.
  - 10. The process according to claim 8, wherein the bacteria are used in which the metabolic pathways which reduce the formation of L-lysine are at least partially suppressed.
- 30 11. The process according to claim 8, wherein coryneform bacteria are used which produce L-lysine.

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5	12.1	the	lysC	gene,	which	encodes	а	feed	back
		resistant aspart			ctate k	cinase,			

- 12.2 the asd gene, which encodes aspartate semialdehyde dehydrogenase,
- the dapA gene, which encodes 12.3 dihydropicolinate synthase,
  - 12.4 the dapB gene, which encodes dihydrodipicolinate reductase,
  - the dapD gene, which encodes 12.5 tetrahydropicolinate succinylase,
- 15 12.6 the dapE gene, which encodes Nsuccinyldiaminopimelate desuccinylase,
  - 12.7 the dapF gene, which encodes diaminopimelate epimerase,
- the lysA gene, which encodes diaminopimelate 12.8 20 decarboxylase,
  - 12.9 the ddh gene, which encodes diaminopimelate dehydrogenase,
  - 12.10 the lysE gene, which encodes lysine export,
  - 12.11 the pyc gene, which encodes pyruvate carboxylase,
    - 12.12 the mgo gene, which encodes malate:quinone oxidoreductase,
    - the zwa1 gene 12.13

12.14 the gdh gene, which encodes glutamate dehydrogenase,

are simultaneously enhanced, over-expressed or amplified.

- 5 13. The process according to claim 8, wherein the bacteria are fermented for the production of L-lysine in which one or more of the genes selected from the group consisting of
- 13.1 the pck gene, which encodes phosphoenolpyruvate carboxykinase,
  - 13.2 the pgi gene, which encodes glucose 6phosphate isomerase,
  - the poxB gene, which encodes pyruvate oxidase,
- 15 13.4 the zwa2 gene,
  - 13.5 the sucC or sucD genes, which encode succinyl CoA synthetase

is/are simultaneously attenuated.

- 14. A process according to one of claims 8-13, wherein
  20 microorganisms of the genus Corynebacterium glutamicum
  are used.
  - 15. A hybridization probe comprising a polynucleotide sequence according to claim 1.
- 16. A method for isolating cDNA which encodes the product of the dapC gene comprising contacting the hybridization probe of claim 15 with a sample.
  - 17. A method for isolation of cDNA or genes which exhibit a high level of similarity with the sequence of the dapC gene comprising contacting a hybridization probe according to claim 15 with a sample.

- 18. DNA originating from coryneform bacteria which encodes N-succinylaminoketopimelate transaminase, in which the amino acid sequence shown in SEQ ID no. 2 in position 209 is replaced with another amino acid, with the exception of L-proline.
- 19. DNA according to claim 18, wherein the amino acid L-proline in position 209 of the enzyme protein (SEQ ID no. 2) is replaced with L-leucine (SEQ ID no. 4).
- 20. DNA according to claim 18, wherein the replacement of L-proline with L-leucine in position 209 is effected by the replacement of the nucleobase cytosine in position 716 with thymine, as shown in SEQ ID no. 3.
  - 21. Coryneform bacteria which contain DNA according to claim 17, 18 or 19.